



SEQUENCE LISTING

<110> Itadani, Hiraku
Takimura, Tetsuo
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<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP)
BINDING PROTEIN-COUPLED RECEPTOR PROTEINS

<130> 06501-083001

<140> 09/891,053
<141> 2001-06-25

<150> PCT/JP99/07280
<151> 1999-12-24

<150> PCT/JP98/05967
<151> 1998-12-25

<150> JP 11/145661
<151> 1999-05-25

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> PRT
<213> Rattus norvegicus

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Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
20 25 30
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
35 40 45
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
50 55 60
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
85 90 95
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
100 105 110
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
115 120 125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130	135	140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp		
145	150	155
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr		160
165	170	175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe		
180	185	190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe		
195	200	205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn		
210	215	220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly		
225	230	235
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro		240
245	250	255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu		
260	265	270
His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu		
275	280	285
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg		
290	295	300
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg		
305	310	315
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly		320
325	330	335
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys		
340	345	350
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu		
355	360	365
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His		
370	375	380
Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu		
385	390	395
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys		400
405	410	

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<211> 1239
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1) ... (1239)

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Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu		
1	5	10
		15
gcc gga gag gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc		96
Ala Gly Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala		
20	25	30
tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca		144
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr		
35	40	45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tgg agc Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser	50	55	60	192
ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp	65	70	75	240
ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu	85	90	95	288
acc ggc cgt tgg acc ttc ggc cggtt ctc tgc aag ctg tgg ctg gtg Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val	100	105	110	336
gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile	115	120	125	384
agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala	130	135	140	432
cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp	145	150	155	480
gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr	165	170	175	528
ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe	180	185	190	576
ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe	195	200	205	624
acg ccc ttc ctc agc gtt acc ttc ttc aac ctc acg atc tac ctg aac Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn	210	215	220	672
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly	225	230	235	720
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro	245	250	255	768
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu	260	265	270	816

cac	agc	tct	ggc	agc	tcc	tca	agg	ggc	act	gag	agg	cca	cgc	tca	ctc		864
His	Ser	Ser	Gly	Ser	Ser	Arg	Gly	Thr	Glu	Arg	Pro	Arg	Ser	Leu			
275						280								285			
aaa	agg	ggc	tcc	aag	cca	tca	gca	tct	tca	gca	tcc	ctg	gag	aag	cgc		912
Lys	Arg	Gly	Ser	Lys	Pro	Ser	Ala	Ser	Ser	Ala	Ser	Leu	Glu	Lys	Arg		
290						295						300					
atg	aag	atg	gtg	tcc	cag	agc	atc	acc	cag	cgc	ttc	cg	ctg	tcg	cg		960
Met	Lys	Met	Val	Ser	Gln	Ser	Ile	Thr	Gln	Arg	Phe	Arg	Leu	Ser	Arg		
305						310					315			320			
gac	aag	aag	gtg	gcc	aag	tcg	ctg	gcc	atc	atc	gtg	agc	atc	ttt	ggg		1008
Asp	Lys	Lys	Val	Ala	Lys	Ser	Leu	Ala	Ile	Ile	Val	Ser	Ile	Phe	Gly		
						325					330			335			
ctc	tgc	tgg	gcg	ccg	tac	acg	ctc	cta	atg	atc	atc	cga	gct	gct	tgc		1056
Leu	Cys	Trp	Ala	Pro	Tyr	Thr	Leu	Leu	Met	Ile	Ile	Arg	Ala	Ala	Cys		
						340					345			350			
cat	ggc	cgc	tgc	atc	ccc	gat	tac	tgg	tac	gag	acg	tcc	ttc	tgg	ctt		1104
His	Gly	Arg	Cys	Ile	Pro	Asp	Tyr	Trp	Tyr	Glu	Thr	Ser	Phe	Trp	Leu		
						355					360			365			
ctg	tgg	gcc	aac	tcg	gcc	gtc	aac	ccc	gtc	ctc	tac	cca	ctg	tgc	cac		1152
Leu	Trp	Ala	Asn	Ser	Ala	Val	Asn	Pro	Val	Leu	Tyr	Pro	Leu	Cys	His		
						370					375			380			
tac	agc	ttc	cgc	aga	gcc	ttc	acc	aag	ctc	ctc	tgc	ccc	cag	aag	ctc		1200
Tyr	Ser	Phe	Arg	Arg	Ala	Phe	Thr	Lys	Leu	Leu	Cys	Pro	Gln	Lys	Leu		
						385					390			395			400
aag	gtc	cag	ccc	cac	ggc	tcc	ctg	gag	cag	tgc	tgg	aag					1239
Lys	Val	Gln	Pro	His	Gly	Ser	Leu	Glu	Gln	Cys	Trp	Lys					
						405					410						

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 3
batngccaaac ctbkcccttct c

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1) ... (20)

<223> n = A,T,C or G

<400> 4

ccataaaaagn nggggttgac

20

<210> 5

<211> 2700

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (351) ... (1589)

<221> misc_feature

<222> (1) ... (2700)

<223> n = A,T,C or G

<400> 5

aattcggcac	gagcgcccag	atcgccccgc	gcactcggtt	gchgctgag	ctagggggtgc	60
accgacgac	cgcggccgc	tggagctcg	ctttgtctc	gtgcagcag	ccgcgcggcc	120
cgcggccactc	cgctcagatt	ccgacaccag	ccccctctgg	atcgcccccc	tggactctag	180
cccgccgtct	tgcctccgacc	ccgcgggacca	tgctccgggc	cccccccega	aaaccgggct	240
ggcgaaagag	ccggcaaaga	ttaggctcac	gagcgccccgc	cccacccggc	caccagctc	300
tccggccgtg	ccctgccccgg	tgtccccgag	ccgtgtgagc	ctgctgggcc	atg gag	356

Met Glu

1

cgc	gcg	ccg	ccc	gac	ggg	ctg	atg	aac	gcg	tcg	ggc	act	ctg	gcc	gga
Arg	Ala	Pro	Pro	Asp	Gly	Leu	Met	Asn	Ala	Ser	Gly	Thr	Leu	Ala	Gly

5	10	15
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404

gag	gag	gag	gct	gca	ggc	ggg	gag	cg	gg	ttc	tcg	gct	gcc	tgg	acc	
Glu	Ala	Ala	Ala	Ala	Gly	Gly	Ala	Arg	Gly	Ala	Arg	Gly	Thr	Ala	Ala	Trp

20	25	30
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452

gct	gtc	ctg	gct	gag	ctc	atg	gag	ctg	ctc	atc	gtg	gcc	aca	gta	ctg
Ala	Val	Leu	Ala	Leu	Met	Ala	Leu	Leu	Ile	Val	Ala	Thr	Val	Leu	

35	40	45	50
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500

ggc	aac	gag	ctg	atg	ctc	gcc	ttc	gtg	gag	atc	tcg	agc	ctc	cgc
Gly	Asn	Ala	Leu	Val	Met	Leu	Ala	Phe	Val	Ala	Asp	Ser	Ser	Leu

55	60	65
----	----	----

548

acc	cag	aac	aac	ttc	ttt	ctg	ctc	aat	ctc	gcc	atc	tcc	gac	ttc	ctc
Thr	Gln	Asn	Asn	Phe	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Phe	Leu

70	75	80
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596

gtg	ggt	gcc	ttc	tgc	atc	cca	ttg	tac	gta	ccc	tat	gtg	ctg	acc	ggc
Val	Gly	Ala	Phe	Cys	Ile	Pro	Leu	Tyr	Val	Pro	Tyr	Val	Leu	Thr	Gly

85	90	95
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644

rgt tgg acc ttc ggc cggtc tgc aag ctg tgg ctg gtg gta gac Arg Trp Thr Phe Gly Arg Gly Leu Cys Leu Trp Leu Val Val Asp 100 105 110	692
tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat Pyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr 115 120 125 130	740
gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln 135 140 145	788
ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu 150 155 160	836
gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser 165 170 175	884
ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr 180 185 190	932
aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro 195 200 205 210	980
ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag Phe Leu Ser Val Thr Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln 215 220 225	1028
agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu 230 235 240	1076
ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc agc tgc Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys 245 250 255	1124
tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser 260 265 270	1172
tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc aaa agg Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg 275 280 285 290	1220
ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc atg aag Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg Met Lys 295 300 305	1268
atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg gac aag Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg Asp Lys 310 315 320	1316
aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg ctc tgc	1364

Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys			
325	330	335	
tgg ggg ccc tac acg ctc cta atg atc atc cga gct gct tgc cat ggc			1412
Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys His Gly			
340	345	350	
cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt ctg tgg			1460
Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp			
355	360	365	370
gcc aac tcc gcc gtc aac ccc gtc ctc tac cca ctg tgc cac tac agc			1508
Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser			
375	380	385	
tcc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag stc aag gtc			1556
Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val			
390	395	400	
cag ccc cac ggc tcc ctg gag cag tgc tgg aag tgaggactg cccccaccctt			1609
Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys			
405	410		
ctgaggccag gcccttgtac ttgtttgagt gggcagccgg agcggtggcg gggccctgg			1669
ccatgcgtccg ctccaaatgc catggcgcc tcttagatca tcaaccccgcc agtggggtag			1729
catggcagggt gggccaagag ccctagttgg tggagctaga gtgtgtgtgt tagctctgcc			1789
gcacattct cttcaccac acagaagaga caatccagga gtcccaggca tgccttccac			1849
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aaaaaaaaaaa a			2700

<210> 6

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 6

cgaggatccg tgaggctccg gtgcccgtc

29

<210> 7

<211> 32

<212> DNA

ccctcgcca	ccgcctgctc	tggccccggc	cccggccccc	ggaccatgc	gttggggccc	180
cccagggaa	cccgacccgg	ccaaaggccc	gaaaagacga	gcctcccggg	ccggggcccc	240
tcccggccgc	ccagctctcg	ggcgggggcc	tgcgggggt	cccgagccg	cgtgagccgt	300
cgggggccatg	gagcggcgcgc	ccgggggggg	gggggtggaa	gttcgggggg	cgctgggggg	360
cgaggcggcg	gggggggggg	gggggggggg	tttcggca	gcctggaccc	gggtgtggc	420
cgcgctcatg	gcgtgtctca	tctggggccac	ggtggtggggc	aacgcgttgg	tcatgtcgcc	480
cttcgtggcc	gactcgagcc	tcggcaccca	gaacaacttc	ttctgtctca	acctcgccat	540
ctccgacttc	ctcgctggta	aatccccagg	ccctggccgc	ttggggaccca	ggggcgccca	600
gctgtggccgg	gccagggggg	actggaaacac	ggacctgggt	ggctcccgca	ggcacacggc	660
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cgaagtctct	tgccactcg	gcctggggac	aggggggtggg	gagagatgtc	cccgggaaagg	780
gacacgggca	ctggggcgagg	cgcaaggggc	aaaggcaggg	ggtgcagctc	tggctctgc	840
gctgttagcca	aacaaaggct	gtgtgggact	taggacggcgc	ggagggcgca	gtggggcggt	900
ttagagaagg	tctgggggag	gggacatgg	agggggattt	ttagagctgt	gttgggggaa	960
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caggctctgc	tgccggctgg	gggggggggg	acgggggggg	gctggagcgc	ccagacacct	1080
gttggggctg	tgaggtgtgt	ctcccaagac	ctcccaagcc	gcttggcagt	agttagtagcg	1140
gctggccgct	ggcggtgc	accaagtgc	cttcaagcca	ggagaaagc	tttctccttg	1200
tctaagctga	gaccgggggt	tgtccagcgc	cagggttaggg	gctggagttc	agcgggggag	1260
gggagaagga	aattgttetc	tttctctt	tgagggctgg	gagggtctg	cagaagtc	1320
gggaatcccg	actccaggct	ctcggggggtc				1380

<210> 12

<211> 448

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (259) ... (425)

<400> 12

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agggggtggta	agatgaggat	ggctagttcc	agaaaagcag	ccaccatgt	accccaggtc	180
ccgcccgtgt	ctgcgtttag	gtccgtctgt	ccctggccccc	ctggctgcat	ggtcccactg	240
tggccctact	ccccacaggc	gcctctgca	tcccactgt	tgtaccctac	gtgctgacag	300
gccgctggac	cttcggccgg	gcctctgca	agctgtggct	gttagtggac	tacctgtgt	360
gcacctctc	tgccttcaac	atcgctctca	tca	ccgttctgt	tcggtcaccc	420
gagcggtgag	tcctggctg	cgagagtc				480

<210> 13

<211> 1893

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (293) ... (1209)

<400> 13

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agtggggagg	gttagaggaa	gggaggggaa	agaggagggg	agggaggaca	ggaggggaaa	180
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cccagcccaa	tattccttcc	gcggggcccc	tgaccagct	gcccttctgc	aggctctata	300
ccggggccag	cagggtgaca	cgccggggcc	agtgcggaaag	atgcgtgtgg	tgtgggtgt	360

ggccttcctg ctgtacggac cagccatctt gagctgggag tacctgtcg ggggcagtc	420
catccccgag gcccaactgt atggcgagtt ttatataaac tggtaatttc tcatacacggc	430
tcccaacctg gagttttta cggcccttccat caggttacc tttttaaacc tcagcatcta	540
cctgaacatc cagaggcgca cccgccttcg gtggatggg gtggagagg cagccggccc	600
cgagccccct cccgaggccc agcccteacc acccccaacc ctgggtgtgt ggggtctgt	660
ggagaagggg cacggggagg ccatgcgggt jccatgggtat ggggtgggtg aggccggcgt	720
aggcgctgag gcccggggagg cgacccttcgg gggtgggtgt ggggggggtt ccgtggcttc	780
accacaccccttcc agctccggca gctcttcggag gggacttgag agggccgcgt cactcaagag	840
gggttccaaag ccatggcggt cctcggttcc actggaaagg ccgtatgaaga tggtgtccca	900
gagtttccacc cagcgcttcc ggctgttcgtt ggacaggaaa gtggcaagt cgctggcgt	960
cattgtgac atctttggc tctgttggc cccatatacg ctgtgtatgt tcatccggc	1020
ccgttgcacat ggccactgcg tccctgacta ctggtaaagaa aacttttctt ggctctgt	1080
ggccaaactcg gctgtcaacc ctgttcttta cccttgcgttcc accacacgtt tccggggc	1140
cttccaccaag ctgtctgtcc cccagaagat caaaatccatcc accacacgtt ccctggagca	1200
ctgttggaaag tgagtggccc accagagctt cccttgcgttcc acccttcgttcc agccaggc	1260
tcttggcatt ctggccctgc tgccccctac ccggctgttcc accccagggg tgagccccgc	1320
cggttctgtg gcccctctt aatggccacgg cccatggagg ccgttccatggagg ccgttccatgg	1380
gjttggccag agggcccttc actggcttggaa ctggagggtt ggtggccggc cctggccccc	1440
acattctggc tccaccggga gggacagtctt ggagggttcc accatgtgtcc ccaccctgt	1500
ctggtgcacca cccttcgcgtt ccacttgcgtt ccgttccatggagg ccgttccatggagg	1560
gttccaggctt ccctggccat gcagtttgc tctgtatgttcc accacacgtt cacaccctgt	1620
ccacacacgtt cacaccgtcc ctctcccccgg accacacgtt ccacacacgtt cacaccctgt	1680
ctgttcttttgc cataaggcctc aggcctggcc ttttccacc ttttccacc accatcttctt	1740
ggcccccggggaa gtgtcaaggg gccccttagaa cccttgcgtt ccgttccatggagg ccgttccatggagg	1800
gggttctttc agaaagatga agaagaaaac atgttgcgttcc accatgtatgtt ccgttccatggagg	1860
ttaatcaaga gagacaaaat tgctgaggag ctc	1893

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 14

tgaacgcttc gggggcgctg

20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 15

gagatggcga gtttgcgttcc accacacgtt ccacacacgtt cacaccctgt

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 16
 ggctccaagg catcgccgtc 20

 <210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> artificially synthesized primer sequence

 <400> 17
 ctcaacttcca gcagtgtcc 20

 <210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> artificially synthesized primer sequence

 <400> 18
 gctctccgcac ccagaacaac 20

 <210> 19
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> artificially synthesized primer sequence

 <400> 19
 tgccgccttg gatgttcag 19

 <210> 20
 <211> 453
 <212> PRT
 <213> Homo sapiens

 <400> 20
 Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu
 1 5 10 15
 Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30
 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45
 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 50 55 60
 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 85 90 95
 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
 100 105 110
 Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115	120	125
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala		
130	135	140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp		
145	150	155
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr		
165	170	175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe		
180	185	190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe		
195	200	205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn		
210	215	220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala		
225	230	235
Gly Pro Glu Pro Pro Pro Glu Ala Gln Pro Ser Pro Pro Pro Pro		
245	250	255
Gly Cys Trp Gly Cys Trp Gln Lys Gly His Gly Glu Ala Met Pro Leu		
260	265	270
His Arg Tyr Gly Val Gly Glu Ala Ala Val Gly Ala Glu Ala Gly Glu		
275	280	285
Ala Thr Leu Gly Gly Gly Gly Gly Ser Val Ala Ser Pro Thr		
290	295	300
Ser Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu		
305	310	315
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg		
325	330	335
Met Lys Met Val Ser Gln Ser Phe Thr Gln Arg Phe Arg Leu Ser Arg		
340	345	350
Asp Arg Lys Val Ala Lys Ser Leu Ala Val Ile Val Ser Ile Phe Gly		
355	360	365
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys		
370	375	380
His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu		
385	390	395
Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His		
405	410	415
His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu		
420	425	430
Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys		
435	440	445
Lys Lys Thr Cys Leu		
450		

<210> 21
<211> 2050
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (271)...(1629)

<400> 21
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gtgagtgtgc ttgggtgacg cttaggcgcc cctccgcagt gcgcgcagga aagcgcactg 120
aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggctccg tcgcggagtc 180

gctgagtcgg tgcctttta gtttagttctg cagtctagta tggccccat ttgccttcc		240	
actcccgagg ccgcgtgac ctgcggggcc atg gag cgc gcg ccg gac ggg		294	
Met Glu Arg Ala Pro Pro Asp Gly			
1	5		
ccg ctg aac gct tcg ggg gcg ctg gcg ggc gag gcg gcg gcg ggc		342	
Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Gly			
10	15	20	
ggg gcg cgc ggc ttc tcg gca gcc tgg acc gcg gtg ctg gcc gcg ctc		390	
Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu			
25	30	35	40
atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg		438	
Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met			
45	50	55	
ctc gcc ttc gtg gcc gac tcg agc ctc cgc acc cag aac aac ttc ttc		486	
Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe			
60	65	70	
ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc gcc gcc ttc tgc atc		534	
Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile			
75	80	85	
cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cg		582	
Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg			
90	95	100	
ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc		630	
Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser			
105	110	115	120
tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg tgc gtc		678	
Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val			
125	130	135	
acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca		726	
Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala			
140	145	150	
gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga		774	
Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly			
155	160	165	
cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc		822	
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro			
170	175	180	
gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc		870	
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile			
185	190	195	200
acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc		918	
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe			
205	210	215	

ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg 220 225 230	956
ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Glu Ala 235 240 245	1014
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag Gln Pro Ser Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys 250 255 260	1062
ggg cac ggg gag gcc atg ccg ctg cac agg tat ggg gtg ggt gag gcg Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala 265 270 275 280	1110
gcc gta ggc gct gag gcc ggg gag gcg acc ctc ggg ggt ggc ggt ggg Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly 285 290 295	1158
ggc ggc tcc gtg gct tca ccc acc tcc agc tcc ggc agc tcc tcg agg Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Gly Ser Ser Ser Arg 300 305 310	1206
ggc act gag agg ccg cgc tca ctc aag agg ggc tcc aag ccg tcg gcg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala 315 320 325	1254
tcc tcg gcc tcg ctg gag aag cgc atg aag atg gtg tcc cag agc ttc Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe 330 335 340	1302
acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tcg ctg Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu 345 350 355 360	1350
gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu 365 370 375	1398
ctg atg atc atc cgg gcc gcc tgc cat ggc cac tgc gtc cct gac tac Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr 380 385 390	1446
tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tcg gct gtc aac Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn 395 400 405	1494
cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr 410 415 420	1542
aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu 425 430 435 440	1590
gag cac tgc tgg aaa aag atg aag aag aaa aca tgt ctg tgaacttgat	1639

Glu His Cys Trp Lys Lys Met Lys Lys Thr Cys Leu
 445 450

gttcctggga	tgttaatca	agagagacaa	aattgctgag	gagctcaggg	ctggattggc	1699
agggtgtggc	tcccacgccc	tcctccctcc	gctaaggctt	cgggtqago	tgtgccagct	1759
gtttctgccc	accccgccctc	tgggctcaca	ccagccctgg	tggccaaggc	tgcggggcc	1819
actctgtttg	ctcacccagg	acctctgggg	gttgtggga	ggggggggcc	ggctggggcc	1879
cgagggtccc	aaggcggtca	ggggcggtcc	agaggagggtg	ccccgggcagg	ggccgcttcg	1939
ccatgtgtgt	tgcacccgtg	ccacgcgttc	tgcatgttgt	tatgttgtgc	cccgctgcgc	1999
tgcctgcaa	accgtgaggt	cacaataaag	tgtattttt	tatttgtgt	g	2050

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 22

tgcatccat tgtacgtncc

20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<221> misc_feature

<222> (1)...(20)

<223> n = A,T,C or G

<400> 23

atcattagga gcgtgtangg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> artificially synthesized primer sequence

<400> 24

tgctctggga caccatcttc

20

<210> 25

<211> 445

<212> PRT

<213> Rattus norvegicus

<400> 25

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1 5 10 15
 Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30
 Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45
 Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 50 55 60
 Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 85 90 95
 Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
 100 105 110
 Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile
 115 120 125
 Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala
 130 135 140
 Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
 145 150 155 160
 Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
 165 170 175
 Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
 180 185 190
 Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
 195 200 205
 Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
 210 215 220
 Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
 225 230 235 240
 Pro Glu Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
 245 250 255
 Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
 260 265 270
 His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu
 275 280 285
 Ala Ala Leu Gly Gly Ser Gly Gly Ala Ala Ala Ser Pro Thr
 290 295 300
 Ser Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
 305 310 315 320
 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
 325 330 335
 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
 340 345 350
 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
 355 360 365
 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
 370 375 380
 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
 385 390 395 400
 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His
 405 410 415
 Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu
 420 425 430
 Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys
 435 440 445

<210> 26
<211> 1953
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (302) ... (1636)

<400> 26					
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gccgcgcgc cccgcggact ccgctcagat tccgacacca gccccctctg gategcgcgc					120
ctggactcta gcccggggtc ttgctccgac cccgcggacc atgctccggg cgccccccgg					180
aaaaccgggc tgggcgaaga gccggcaaag attaggtctca cgagcggggg ccccacccgg					240
ccacccagct ctccgcgggt gcctgccccg gtgtccccga gccgtgtgag cctgtggc					300
c atg gag cgc gcg ccc gac ggg ctg atg aac gcg tcg ggc act ctg					349
Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu					
1 5 10 15					
gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc					397
Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala					
20 25 30					
tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca					445
Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr					
35 40 45					
gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc					493
Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser					
50 55 60					
ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac					541
Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp					
65 70 75 80					
ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg					589
Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu					
85 90 95					
acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg					637
Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val					
100 105 110					
gta gac tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc					685
Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile					
115 120 125					
agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc					733
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala					
130 135 140					
cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg					781
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp					
145 150 155 160					
gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac					829

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr			
165	170	175	
ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc			877
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe			
180	185	190	
tcc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc			925
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe			
195	200	205	
acg ccc ttc ctc acg gtt acc ttc ttc aac ctc acg atc tac ctg aac			973
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn			
210	215	220	
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc			1021
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly			
225	230	235	240
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc			1069
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro			
245	250	255	
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg			1117
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu			
260	265	270	
cac agg tat ggg gtg ggt gag gca ggc cct ggt gtt gag gct ggg gag			1165
His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu			
275	280	285	
gct gcc ctc ggg ggt ggc agt ggt gga ggt gct gct gcc tcg ccc acc			1213
Ala Ala Leu Gly Gly Ser Gly Gly Ala Ala Ala Ser Pro Thr			
290	295	300	
tcc agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc			1261
Ser Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu			
305	310	315	320
aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc			1309
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg			
325	330	335	
atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg			1357
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg			
340	345	350	
gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg			1405
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly			
355	360	365	
ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc			1453
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys			
370	375	380	
cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt			1501
His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu			

335	390	395	400	
ctg tgg gcc aac tcg gcc gtc aac ccc gtc	ctc tac cca	ctg tgc cac		1549
Leu Trp Ala Asn Ser Ala Val Asn Pro Val	Leu Tyr Pro Leu Cys His			
405	410		415	
tac agc ttc cgc aga gcc ttc acc aag	ctc ctc tgc ccc cag aag ctc			1597
Tyr Ser Phe Arg Arg Ala Phe Thr Lys	Leu Cys Pro Gln Lys Leu			
420	425		430	
aag gtc cag ccc cac ggc tcc ctg gag cag	tgc tgg aag tgagcagctg			1646
Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys				
435	440		445	
ccccaccctt ctgaggccag gcccttgtac ttgtttgagt	gggcagccgg agcggtggcg			1706
gggccttgtt ccatgctccg ctccaaatgc catggggcc	tcttagatca tcaaccccg			1766
agtggggtag catggcaggt gggccaagag ccctagttgg	tggagataga gtgtgctgg			1826
tagctctgcc gcacattctc cttcaccaca cagaagagac	aatccaggag tcccaggcat			1886
gccttcacct acacacacac acacacacac acacacacac	acacacacat gcagtgccag			1946
tgtatgtc				1953